

SEQUENCE LISTING

019114
10 Rec'd Patent 20 MAY 2004

<110> Seishi KATO

Tomoko KIMURA

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 1997.13000

<140> US 10/019,114

<141> 2000-06-16

<150> JP 11-188835

<151> 1999-07-02

<160> 30

<210> 1

<211> 233

<212> PRT

<213> Homo sapiens

<400> 1

Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu Leu Leu Gly Ser

1 5 10 15

Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn Pro Glu Ala Asn

20 25 30

Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr Pro Tyr Glu Glu

35 40 45

Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly Ile Tyr Arg Ile

50 55 60

Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro Lys Pro Ala Val
 65 70 75 80
 Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn Trp Ile Cys Asn
 85 90 95
 Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp Ser Gly Tyr Asp
 100 105 110
 Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Leu
 115 120 125
 Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe Ser Leu Asp Glu
 130 135 140
 Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe Ile Ile Glu Lys
 145 150 155 160
 Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser Gln Gly Thr Thr
 165 170 175
 Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu Ala Lys Lys Ile
 180 185 190
 Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val Lys Tyr Thr Gln
 195 200 205
 Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg Val Val Lys Val
 210 215 220
 Cys Asp Phe Pro Ser Phe Asn Leu Lys
 225 230

<210> 2

<211> 273

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala

1	5	10	15
Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala			
20	25	30	
Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val			
35	40	45	
Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr			
50	55	60	
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala			
65	70	75	80
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser			
85	90	95	
Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg			
100	105	110	
Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly			
115	120	125	
Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg			
130	135	140	
Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp			
145	150	155	160
Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys			
165	170	175	
Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val			
180	185	190	
Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp			
195	200	205	
Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu			
210	215	220	
Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu			
225	230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln			

	245	250	255
Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp			
	260	265	270

Ser

<210> 3

<211> 282

<212> PRT

<213> Homo sapiens

<400> 3

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu			
1	5	10	15
Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro			
	20	25	30
Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu			
	35	40	45
Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr			
	50	55	60
Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys			
65	70	75	80
Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp			
	85	90	95
Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala			
	100	105	110
Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys			
	115	120	125
Arg Ser Glu Asn Lys Asn Glu Gly Gln Asp Ala Thr Met Tyr Cys Lys			
	130	135	140
Ser Val Gly Tyr Pro His Pro Asp Trp Ile Trp Arg Lys Lys Glu Asn			
145	150	155	160

Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe Ile Ile			
	165	170	175
Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln Ile Thr			
	180	185	190
Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile Gly Ser			
	195	200	205
Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala Pro Leu			
	210	215	220
Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val Val Ile			
225	230	235	240
Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro Asp Asp			
	245	250	255
Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn His Lys			
	260	265	270
Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn			
	275	280	

<210> 4

<211> 238

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Leu Asn Glu His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu			
1	5	10	15
Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu			
	20	25	30
Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala			
	35	40	45
Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr			
50	55	60	

Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys
 65 70 75 80
 Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser
 85 90 95
 Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala
 100 105 110
 Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val
 115 120 125
 Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly
 130 135 140
 Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn
 145 150 155 160
 Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser
 165 170 175
 Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Val
 180 185 190
 His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln
 195 200 205
 Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp
 210 215 220
 His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
 225 230 235

<210> 5

<211> 372

<212> PRT

<213> Homo sapiens

<400> 5

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro

1	5	10	15
Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val			
20	25	30	
Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu			
35	40	45	
Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu			
50	55	60	
Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser			
65	70	75	80
Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr			
85	90	95	
Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu			
100	105	110	
Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg			
115	120	125	
Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly			
130	135	140	
Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His			
145	150	155	160
Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe			
165	170	175	
Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val			
180	185	190	
Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val			
195	200	205	
Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr			
210	215	220	
Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu			
225	230	235	240
Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val			

245	250	255
Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg		
260	265	270
Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala		
275	280	285
Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe		
290	295	300
Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser		
305	310	315
Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala		
325	330	335
Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu		
340	345	350
Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln		
355	360	365
Asp Ser Ala Leu		
370		

<210> 6

<211> 146

<212> PRT

<213> Homo sapiens

<400> 6

Met Trp Lys Leu Trp Arg Ala Glu Glu Gly Ala Ala Ala Leu Gly Gly		
1	5	10
Ala Leu Phe Leu Leu Leu Phe Ala Leu Gly Val Arg Gln Leu Leu Lys		
20	25	30
Gln Arg Arg Pro Met Gly Phe Pro Pro Gly Pro Pro Gly Leu Pro Phe		
35	40	45

Ile Gly Asn Ile Tyr Ser Leu Ala Ala Ser Ser Glu Leu Pro His Val

50

55

60

Tyr Met Arg Lys Gln Ser Gln Val Tyr Gly Glu Val Gln Pro Arg Arg

65

70

75

80

Ala Pro Gly Arg Glu Gly Arg Gln Ala Gly Pro Gly Trp Pro Gly Pro

85

90

95

Ser Trp Leu Asp Leu Trp Pro Pro Leu Gly Arg Leu Val Gly Thr Ser

100

105

110

Pro Cys Ala Gly Cys Pro Leu Arg Asp Thr Arg Phe Pro Gly Leu Glu

115

120

125

Gly Arg Ser Pro Arg Arg Arg Ala Pro Leu Gln Gly Glu Pro Arg Pro

130

135

140

Cys Arg

145

<210> 7

<211> 302

<212> PRT

<213> Homo sapiens

<400> 7

Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val

1

5

10

15

Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu

20

25

30

Cys Leu Ala Thr Cys Leu Asp His His Phe Pro Thr Gly Ser Arg Pro

35

40

45

Thr Val Pro Gly Pro Leu His Phe Ser Gly Tyr Ser Ser Val Pro Asp

50

55

60

Gly Lys Pro Leu Val Arg Glu Pro Cys Arg Ser Cys Ala Val Val Ser

65	70	75	80
Ser Ser Gly Gln Met Leu Gly Ser Gly Leu Gly Ala Glu Ile Asp Ser			
85	90	95	
Ala Glu Cys Val Phe Arg Met Asn Gln Ala Pro Thr Val Gly Phe Glu			
100	105	110	
Ala Asp Val Gly Gln Arg Ser Thr Leu Arg Val Val Ser His Thr Ser			
115	120	125	
Val Pro Leu Leu Leu Arg Asn Tyr Ser His Tyr Phe Gln Lys Ala Arg			
130	135	140	
Asp Thr Leu Tyr Met Val Trp Gly Gln Gly Arg His Met Asp Arg Val			
145	150	155	160
Leu Gly Gly Arg Thr Tyr Arg Thr Leu Leu Gln Leu Thr Arg Met Tyr			
165	170	175	
Pro Gly Leu Gln Val Tyr Thr Phe Thr Glu Arg Met Met Ala Tyr Cys			
180	185	190	
Asp Gln Ile Phe Gln Asp Glu Thr Gly Lys Asn Arg Arg Gln Ser Gly			
195	200	205	
Ser Phe Leu Ser Thr Gly Trp Phe Thr Met Ile Leu Ala Leu Glu Leu			
210	215	220	
Cys Glu Glu Ile Val Val Tyr Gly Met Val Ser Asp Ser Tyr Cys Arg			
225	230	235	240
Glu Lys Ser His Pro Ser Val Pro Tyr His Tyr Phe Glu Lys Gly Arg			
245	250	255	
Leu Asp Glu Cys Gln Met Tyr Leu Ala His Glu Gln Ala Pro Arg Ser			
260	265	270	
Ala His Arg Phe Ile Thr Glu Lys Ala Val Phe Ser Arg Trp Ala Lys			
275	280	285	
Lys Arg Pro Ile Val Phe Ala His Pro Ser Trp Arg Thr Glu			
290	295	300	

<210> 8

<211> 194

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
1 5 10 15
Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
20 25 30
Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
35 40 45
Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
50 55 60
Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
65 70 75 80
Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
85 90 95
Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
100 105 110
Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
115 120 125
Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
130 135 140
Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala
145 150 155 160
Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys
165 170 175
Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His
180 185 190

Gly Phe

<210> 9

<211> 542

<212> PRT

<213> Homo sapiens

<400> 9

Met	Lys	Met	Lys	Ser	Gln	Ala	Thr	Met	Ile	Cys	Cys	Leu	Val	Phe	Phe
1			5						10					15	
Leu	Ser	Thr	Glu	Cys	Ser	His	Tyr	Arg	Ser	Lys	Ile	His	Leu	Lys	Ser
			20					25					30		
Tyr	Ser	Glu	Val	Ala	Asn	His	Ile	Leu	Asp	Thr	Ala	Ala	Ile	Ser	Asn
			35				40					45			
Trp	Ala	Phe	Ile	Pro	Asn	Lys	Asn	Ala	Ser	Ser	Asp	Leu	Leu	Gln	Ser
			50			55					60				
Val	Asn	Leu	Phe	Ala	Arg	Gln	Leu	His	Ile	His	Asn	Asn	Ser	Glu	Asn
			65			70				75				80	
Ile	Val	Asn	Glu	Leu	Phe	Ile	Gln	Thr	Lys	Gly	Phe	His	Ile	Asn	His
				85					90				95		
Asn	Thr	Ser	Glu	Lys	Ser	Leu	Asn	Phe	Ser	Met	Ser	Met	Asn	Asn	Thr
			100					105					110		
Thr	Glu	Asp	Ile	Leu	Gly	Met	Val	Gln	Ile	Pro	Arg	Gln	Glu	Leu	Arg
			115					120					125		
Lys	Leu	Trp	Pro	Asn	Ala	Ser	Gln	Ala	Ile	Ser	Ile	Ala	Phe	Pro	Thr
			130				135					140			
Leu	Gly	Ala	Ile	Leu	Arg	Glu	Ala	His	Leu	Gln	Asn	Val	Ser	Leu	Pro
			145			150				155				160	
Arg	Gln	Val	Asn	Gly	Leu	Val	Leu	Ser	Val	Val	Leu	Pro	Glu	Arg	Leu
				165					170					175	

Gln Glu Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala
 180 185 190
 Arg Ala Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu
 195 200 205
 Lys Ala Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg
 210 215 220
 Cys Asn Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser
 225 230 235 240
 Lys Ser Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu
 245 250 255
 Ser Val Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr
 260 265 270
 Val Trp Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val
 275 280 285
 Cys Ile Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe
 290 295 300
 Ile Ile Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys
 305 310 315 320
 Val Ala Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe
 325 330 335
 Trp Met Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile
 340 345 350
 Phe Arg Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile
 355 360 365
 Gly Tyr Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr
 370 375 380
 Glu Pro Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp
 385 390 395 400
 Asp Asn Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile
 405 410 415

Val Ala Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln

420

425

430

Arg Pro Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met

435

440

445

Arg Ile Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr

450

455

460

Trp Gly Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe

465

470

475

480

His Ile Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu

485

490

495

Leu Phe Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met

500

505

510

Arg Met Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser

515

520

525

Leu Gly Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly

530

535

540

<210> 10

<211> 276

<212> PRT

<213> Homo sapiens

<400> 10

Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu

1

5

10

15

Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro

20

25

30

Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala

35

40

45

Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala

50	55	60
Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser		
65	70	75
Arg Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro		
	85	90
Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp		95
	100	105
Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val		110
	115	120
Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn		125
	130	135
Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met		140
145	150	155
Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile		160
	165	170
Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly		175
	180	185
Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu		190
	195	200
Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe		205
	210	215
Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly		220
225	230	235
Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu		240
	245	250
Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro		255
	260	265
Ser Leu Ser Pro		270
	275	

<210> 11

<211> 699

<212> DNA

<213> Homo sapiens

<400> 11

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atgtggcagc ttttagcagc agcatgctgg atgcttcttc ttggatctat gtatggttat      60
gacaagaaag gaaacaatgc aaaccctgaa gctaatatga atattagcca gattatttct      120
tactgggggtt atccttatga agagtatgat gttacaacaa aagatggtta tatccttgga      180
atztatagga ttccacatgg aagaggatgc ccagggagga cagctccaaa gcctgctgtg      240
tatttgcagc atggcttaat tgcactctgcc agtaactgga ttgcaacct gcccaacaac      300
agtttggctt tccttctggc agatagtggg tatgacgtgt ggttggggaa cagccgagga      360
aacacttggt ccagaaaaca ccttaaattg tcaccgaaat caccagaata ctgggccttc      420
agtttggatg agatggctaa atatgacctt ccagccacaa tcaattttat catagagaaa      480
actggacaga agcgactcta ctacgtgggc cactcacaag gcaccaccat agcttttata      540
gcattttcta caaaccaga actggctaaa aagattaaga ttttttttgc actggctcca      600
gttgtcacag ttaaatacac ccaaagtcct atgaaaaaac taacaaccct ttccaggcga      660
gtagttaagg tatgtgactt cccaagtttt aatctgaaa                               699
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<210> 12

<211> 819

<212> DNA

<213> Homo sapiens

<400> 12

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gagcacgcct accggcccgg ccgtaggggtg tgtgctgtcc gggctcacgg ggaccctgtc      120
tccgagtcgt tcgtgcagcg tgtgtaccag cccttcctca ccacctgcga cgggcaccgg      180
gcctgcagca cctaccgaac catctatagg accgcctacc gccgcagccc tgggctggcc      240
cctgccaggc ctgcctacgc gtgctgcccc ggctggaaga ggaccagcgg gcttcctggg      300
gcctgtggag cagcaatatg ccagccgcca tgccggaacg gagggagctg tgtccagcct      360
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ggccgctgcc gctgccctgc aggatggcgg ggtgacactt gccagtcaga tgtggatgaa	420
tgcagtgcta ggagggggcg ctgtccccag cgctgcgtca acaccgccgg cagttactgg	480
tgccagtgtt gggagggggca cagcctgtct gcagacggta cactctgtgt gccaaggga	540
gggcccccca ggggtggccc caaccgaca ggagtggaca gtgcaatgaa ggaagaagtg	600
cagaggctgc agtccagggt ggacctgctg gaggagaagc tgcagctggt gctggcccca	660
ctgcacagcc tggcctcgca ggcactggag catgggctcc cggaccccg cagcctcctg	720
gtgcactcct tccagcagct cggccgcctc gactccctga gcgagcagat ttccttcctg	780
gaggagcagc tggggtcctg ctctgcaag aaagactcg	819

<210> 13

<211> 846

<212> DNA

<213> Homo sapiens

<400> 13

atgtcgggtt cgtcgctgcc cagcgccctg gccctctcgc tgttgctggt ctctggctcc	60
ctctcccgag ggccaggcgc cgctcagaac gagccaagga ttgtcaccag tgaagaggtc	120
attattcgag acagccctgt tctccctgtc accctgcagt gtaacctcac ctccagctct	180
cacaccctta catacagcta ctggacaaag aatggggtgg aactgagtgc cactcgtaag	240
aatgccagca acatggagta caggatcaat aagccgagag ctgaggattc aggogaatac	300
cactgcgtat atcactttgt cagcgctcct aaagcaaacg ccaccattga agtgaaagcc	360
gctcctgaca tcaactggcca taaacggagt gagaacaaga atgaagggca ggatgccact	420
atgtattgca agtcagttgg ctacccccac ccagactgga tatggcgcaa gaaggagaac	480
gggatgccca tggacattgt caatacctct ggccgcttct tcatcatcaa caaggaaaat	540
tacactgagt tgaacattgt gaacctgcag atcacggaag accctggcga gtatgaatgt	600
aatgccacca acgccattgg ctccgcctct gttgtcactg tcctcagggt gcggagccac	660
ctggccccac tctggccttt cttgggaatt ctggctgaaa ttatcatcct tgtggtgatc	720
attgttgtgt atgagaagag gaagaggcca gatgagggtc ctgacgatga tgaaccagct	780
ggaccaatga aaaccaactc taccaacaat cacaagata aaaacttgcg ccagagaaac	840
acaaat	846

<210> 14

<211> 714

<212> DNA

<213> Homo sapiens

<400> 14

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gccaaagctta aagcctccag ccggacctcg gctctgctct ccggcttcgc catgggtggca    120
atgggtggagg tgcagctgga cgctgaccac gactaccacac cggggctgct catcgcccttc    180
agtgcctgca ccacagtgct ggtggctgtg cacctgtttg cgctcatgat cagcacctgc      240
atcctgcccc acatcgaggc ggtgagcaac gtgcacaatc tcaactcggg caaggagtcc      300
ccccatgagc gcatgcaccg ccacatcgag ctggcctggg ccttctccac cgtcatcggc      360
acgctgctct tcctagctga ggtgggtgctg ctctgctggg tcaagttctt gcccctcaag      420
aagcagccag gccagccaag gcccaccagc aagccccccg ccagtggcgc agcagccaac      480
gtcagcacca gcggcatcac cccgggccag gcagctgcca tcgcctcgac caccatcatg      540
gtgcccttcg gctgatctt tatcgtcttc gccgtccact tctaccgctc actgggttagc      600
cataagaccg accgacagtt ccaggagctc aacgagctgg cggagtttgc ccgcttacag      660
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<210> 15

<211> 1116

<212> DNA

<213> Homo sapiens

<400> 15

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gccgagggct tccgcaacac cctgcgcggc ctgggcactc cgcaccgggc caggacctcg	960
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<210> 16

<211> 438

<212> DNA

<213> Homo sapiens

<400> 16

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ccggggcgc cggggctgcc atttatcggc aacatctatt ccctggcagc ctcatccgag	180
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gccccgggca gggagggccg ccaggctggc ccgggctggc cagggccttc ctggttgagc	300
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<210> 17

<211> 906

<212> DNA

<213> Homo sapiens

<400> 17

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cagatgtacc tggcacacga gcaggcgccc cgaagcgccc accgcttcat cactgagaag      840
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<210> 18

<211> 582

<212> DNA

<213> Homo sapiens

<400> 18

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ggaagacgtc acggcctgaa ctactgtgga gttcgtgctt ctgaaaggct ggctgaaata      180
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gacatgccat acctcctgaa atatcaaccc atgatgcaaa ccattggcca aaagtactgc	240
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tacagtgggg gtgctggcta tgtccgaagc agccaggacc tgagctgtga cttctgcaat	540
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<210> 19

<211> 1626

<212> DNA

<213> Homo sapiens

<400> 19

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<210> 20

<211> 828

<212> DNA

<213> Homo sapiens

<400> 20

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<210> 21

<211> 1308

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)...(777)

<400> 21

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Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu
1 5 10
ctt ctt gga tct atg tat ggt tat gac aag aaa gga aac aat gca aac 159
Leu Leu Gly Ser Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn
15 20 25
cct gaa gct aat atg aat att agc cag att att tct tac tgg ggt tat 207
Pro Glu Ala Asn Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr
30 35 40
cct tat gaa gag tat gat gtt aca aca aaa gat ggt tat atc ctt gga 255
Pro Tyr Glu Glu Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly
45 50 55 60
att tat agg att cca cat gga aga gga tgc cca ggg agg aca gct cca 303
Ile Tyr Arg Ile Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro
65 70 75
aag cct gct gtg tat ttg cag cat ggc tta att gca tct gcc agt aac 351

Lys Pro Ala Val Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn
 80 85 90
 tgg att tgc aac ctg ccc aac aac agt ttg gct ttc ctt ctg gca gat 399
 Trp Ile Cys Asn Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp
 95 100 105
 agt ggt tat gac gtg tgg ttg ggg aac agc cga gga aac act tgg tcc 447
 Ser Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser
 110 115 120
 aga aaa cac ctt aaa ttg tca ccg aaa tca cca gaa tac tgg gcc ttc 495
 Arg Lys His Leu Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe
 125 130 135 140
 agt ttg gat gag atg gct aaa tat gac ctt cca gcc aca atc aat ttt 543
 Ser Leu Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe
 145 150 155
 atc ata gag aaa act gga cag aag cga ctc tac tac gtg ggc cac tca 591
 Ile Ile Glu Lys Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser
 160 165 170
 caa ggc acc acc ata gct ttt ata gca ttt tct aca aac cca gaa ctg 639
 Gln Gly Thr Thr Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu
 175 180 185
 gct aaa aag att aag ata ttt ttt gca ctg gct cca gtt gtc aca gtt 687
 Ala Lys Lys Ile Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val
 190 195 200
 aaa tac acc caa agt cct atg aaa aaa cta aca acc ctt tcc agg cga 735
 Lys Tyr Thr Gln Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg
 205 210 215 220
 gta gtt aag gta tgt gac ttc cca agt ttt aat ctg aaa taacta 780
 Val Val Lys Val Cys Asp Phe Pro Ser Phe Asn Leu Lys
 225 230
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<210> 22

<211> 1272

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)...(881)

<400> 22

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 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
 / 1 5 10 15
 gtg ggc ggc aca gag cac gcc tac cgg ccc ggc cgt agg gtg tgt gct 155
 Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
 20 25 30
 gtc cgg gct cac ggg gac cct gtc tcc gag tcg ttc gtg cag cgt gtg 203
 Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
 35 40 45
 tac cag ccc ttc ctc acc acc tgc gac ggg cac cgg gcc tgc agc acc 251
 Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
 50 55 60

tac	cga	acc	atc	tat	agg	acc	gcc	tac	cgc	cgc	agc	cct	ggg	ctg	gcc	299
Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser	Pro	Gly	Leu	Ala	
65					70				75					80		
cct	gcc	agg	cct	cgc	tac	gcg	tgc	tgc	ccc	ggc	tgg	aag	agg	acc	agc	347
Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	Gly	Trp	Lys	Arg	Thr	Ser	
				85				90					95			
ggg	ctt	cct	ggg	gcc	tgt	gga	gca	gca	ata	tgc	cag	ccg	cca	tgc	cgg	395
Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln	Pro	Pro	Cys	Arg	
		100					105					110				
aac	gga	ggg	agc	tgt	gtc	cag	cct	ggc	cgc	tgc	cgc	tgc	cct	gca	gga	443
Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	
		115				120						125				
tgg	cgg	ggt	gac	act	tgc	cag	tca	gat	gtg	gat	gaa	tgc	agt	gct	agg	491
Trp	Arg	Gly	Asp	Thr	Cys	Gln	Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	
	130					135					140					
agg	ggc	ggc	tgt	ccc	cag	cgc	tgc	gtc	aac	acc	gcc	ggc	agt	tac	tgg	539
Arg	Gly	Gly	Cys	Pro	Gln	Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	
145				150				155					160			
tgc	cag	tgt	tgg	gag	ggg	cac	agc	ctg	tct	gca	gac	ggt	aca	ctc	tgt	587
Cys	Gln	Cys	Trp	Glu	Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	
				165				170					175			
gtg	ccc	aag	gga	ggg	ccc	ccc	agg	gtg	gcc	ccc	aac	ccg	aca	gga	gtg	635
Val	Pro	Lys	Gly	Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	
			180					185					190			
gac	agt	gca	atg	aag	gaa	gaa	gtg	cag	agg	ctg	cag	tcc	agg	gtg	gac	683
Asp	Ser	Ala	Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	
	195						200					205				
ctg	ctg	gag	gag	aag	ctg	cag	ctg	gtg	ctg	gcc	cca	ctg	cac	agc	ctg	731
Leu	Leu	Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	
210						215					220					

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Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu	
1 5 10	
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Leu Leu Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn	
15 20 25 30	
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Glu Pro Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro	
35 40 45	
gtt ctc cct gtc acc ctg cag tgt aac ctc acc tcc agc tct cac acc	373
Val Leu Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr	
50 55 60	
ctt aca tac agc tac tgg aca aag aat ggg gtg gaa ctg agt gcc act	421
Leu Thr Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr	
65 70 75	
cgt aag aat gcc agc aac atg gag tac agg atc aat aag ccg aga gct	469
Arg Lys Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala	
80 85 90	
gag gat tca ggc gaa tac cac tgc gta tat cac ttt gtc agc gct cct	517
Glu Asp Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro	
95 100 105 110	
aaa gca aac gcc acc att gaa gtg aaa gcc gct cct gac atc act ggc	565
Lys Ala Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly	
115 120 125	
cat aaa cgg agt gag aac aag aat gaa ggg cag gat gcc act atg tat	613
His Lys Arg Ser Glu Asn Lys Asn Glu Gly Gln Asp Ala Thr Met Tyr	
130 135 140	
tgc aag tca gtt ggc tac ccc cac cca gac tgg ata tgg cgc aag aag	661
Cys Lys Ser Val Gly Tyr Pro His Pro Asp Trp Ile Trp Arg Lys Lys	

145	150	155	
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Glu Asn Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe			
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Ile Ile Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln			
175	180	185	190
atc acg gaa gac cct ggc gag tat gaa tgt aat gcc acc aac gcc att			805
Ile Thr Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile			
	195	200	205
ggc tcc gcc tct gtt gtc act gtc ctc agg gtg cgg agc cac ctg gcc			853
Gly Ser Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala			
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cca ctc tgg cct ttc ttg gga att ctg gct gaa att atc atc ctt gtg			901
Pro Leu Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val			
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Val Ile Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro			
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Asp Asp Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn			
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cac aaa gat aaa aac ttg cgc cag aga aac aca aat taagtac			1040
His Lys Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn			
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<210> 24

<211> 1260

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147)...(863)

<400> 24

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gggacgggga gccccgggg gccccgccac tgccgcgctc cgccgtcacc taccgggact 120
ggatcggcca gagttactcc gaggtg atg agc ctc aac gag cac tcc atg 170
Met Ser Leu Asn Glu His Ser Met
1 5
cag gcg ctg tcc tgg cgc aag ctc tac ttg agc cgc gcc aag ctt aaa 218

Gln Ala Leu Ser Trp Arg Lys Leu Tyr Leu Ser Arg Ala Lys Leu Lys

10

15

20

gcc tcc agc cgg acc tcg gct ctg ctc tcc ggc ttc gcc atg gtg gca 266

Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala Met Val Ala

25

30

35

40

atg gtg gag gtg cag ctg gac gct gac cac gac tac cca ccg ggg ctg 314

Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro Pro Gly Leu

45

50

55

ctc atc gcc ttc agt gcc tgc acc aca gtg ctg gtg gct gtg cac ctg 362

Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala Val His Leu

60

65

70

ttt gcg ctc atg atc agc acc tgc atc ctg ccc aac atc gag gcg gtg 410

Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile Glu Ala Val

75

80

85

agc aac gtg cac aat ctc aac tcg gtc aag gag tcc ccc cat gag cgc 458

Ser Asn Val His Asn Leu Asn Ser Val Lys Glu Ser Pro His Glu Arg

90

95

100

atg cac cgc cac atc gag ctg gcc tgg gcc ttc tcc acc gtc atc ggc 506

Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val Ile Gly

105

110

115

120

acg ctg ctc ttc cta gct gag gtg gtg ctg ctc tgc tgg gtc aag ttc 554

Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val Lys Phe

125

130

135

ttg ccc ctc aag aag cag cca ggc cag cca agg ccc acc agc aag ccc 602

Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser Lys Pro

140

145

150

ccc gcc agt ggc gca gca gcc aac gtc agc acc agc ggc atc acc ccg 650

Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile Thr Pro

155

160

165

ggc cag gca get gcc atc gcc tcg acc acc atc atg gtg ccc ttc ggc 698

Gly	Gln	Ala	Ala	Ala	Ile	Ala	Ser	Thr	Thr	Ile	Met	Val	Pro	Phe	Gly	
170					175					180						
ctg	atc	ttt	atc	gtc	ttc	gcc	gtc	cac	ttc	tac	cgc	tca	ctg	gtt	agc	746
Leu	Ile	Phe	Ile	Val	Phe	Ala	Val	His	Phe	Tyr	Arg	Ser	Leu	Val	Ser	
185				190					195				200			
cat	aag	acc	gac	cga	cag	ttc	cag	gag	ctc	aac	gag	ctg	gcg	gag	ttt	794
His	Lys	Thr	Asp	Arg	Gln	Phe	Gln	Glu	Leu	Asn	Glu	Leu	Ala	Glu	Phe	
				205				210					215			
gcc	cgc	tta	cag	gac	cag	ctg	gac	cac	aga	ggg	gac	cac	ccc	ctg	acg	842
Ala	Arg	Leu	Gln	Asp	Gln	Leu	Asp	His	Arg	Gly	Asp	His	Pro	Leu	Thr	
		220				225				230						
ccc	ggc	agc	cac	tat	gcc	taggccc	atg	tgg	tct	gggc	ccttcc	agt				890
Pro	Gly	Ser	His	Tyr	Ala											
				235												
ctttggc	ctt	acgc	cccttc	ccttg	acctt	gtc	ctg	cccc	agc	ctcac	gg	acag	cctg	cg		950
caggggg	gctg	ggctt	cagca	agggg	cagag	cgtg	gag	gga	agagg	at	ttt	tata	agaga			1010
atttctg	cac	tttgaa	actg	tctcta	aga	gaata	agcat	ttc	ctgtt	ct	tccag	ctcca				1070
gggccac	ctc	ctgtt	gggag	gcggt	ggggg	gccaa	agtgg	ggccac	acac	tcg	ctgtg	tc				1130
ccctctc	ctc	ccctgt	gcca	gtgcc	acctg	ggtgc	ctc	cctgt	ctgt	ccgt	ctca	ac				1190
ctccctc	ccg	tccag	cattg	agtgt	gtaca	tgtgt	gtgtg	acacata	aat	ata	ctcata					1250
ggacac	ctcc															1260

<210> 25

<211> 1720

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (282)...(1400)

<400> 25

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aggaggtctc tgctgctgat gaagctgtga ccaaaccgac ccaacccttg gcagccatct	120
gtccctgcag ccatagccca cattcccatg acctccctct gcttgttttg ggaccatgtc	180
tgtacagcct ctaggcccca gccccggagg tgaatgccat gccatgattc tgggtgtgctc	240
catggcatcc ccagcctagc tcccaatccc actttggcac g atg tta gcc aac	293

Met Leu Ala Asn

1

agc tcc tca acc aac agt tct gtt ctc ccg tgt cct gac tac cga cct	341
Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro Asp Tyr Arg Pro	
5 10 15 20	
acc cac cgc ctg cac ttg gtg gtc tac agc ttg gtg ctg gct gcc ggg	389
Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val Leu Ala Ala Gly	
25 30 35	
ctc ccc ctc aac gcg cta gcc ctc tgg gtc ttc ctg cgc gcg ctg cgc	437
Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu Arg Ala Leu Arg	
40 45 50	
gtg cac tcg gtg gtg agc gtg tac atg tgt aac ctg gcg gcc agc gac	485
Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu Ala Ala Ser Asp	
55 60 65	
ctg ctc ttc acc ctc tcg ctg ccc gtt cgt ctc tcc tac tac gca ctg	533
Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser Tyr Tyr Ala Leu	
70 75 80	
cac cac tgg ccc ttc ccc gac ctc ctg tgc cag acg acg ggc gcc atc	581
His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr Thr Gly Ala Ile	
85 90 95 100	
ttc cag atg aac atg tac ggc agc tgc atc ttc ctg atg ctc atc aac	629
Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu Met Leu Ile Asn	
105 110 115	
gtg gac cgc tac gcc gcc atc gtg cac ccg ctg cga ctg cgc cac ctg	677

Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg Leu Arg His Leu	
120 125 130	
cgg cgg ccc cgc gtg gcg cgg ctg ctc tgc ctg ggc gtg tgg gcg ctc	725
Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly Val Trp Ala Leu	
135 140 145	
atc ctg gtg ttt gcc gtg ccc gcc gcc cgc gtg cac agg ccc tcg cgt	773
Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His Arg Pro Ser Arg	
150 155 160	
tgc cgc tac cgg gac ctc gag gtg cgc cta tgc ttc gag agc ttc agc	821
Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe Glu Ser Phe Ser	
165 170 175 180	
gac gag ctg tgg aaa ggc agg ctg ctg ccc ctc gtg ctg ctg gcc gag	869
Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val Leu Leu Ala Glu	
185 190 195	
gcg ctg ggc ttc ctg ctg ccc ctg gcg gcg gtg gtc tac tcg tcg ggc	917
Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val Tyr Ser Ser Gly	
200 205 210	
cga gtc ttc tgg acg ctg gcg cgc ccc gac gcc acg cag agc cag cgg	965
Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr Gln Ser Gln Arg	
215 220 225	
cgg cgg aag acc gtg cgc ctc ctg ctg gct aac ctc gtc atc ttc ctg	1013
Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu Val Ile Phe Leu	
230 235 240	
ctg tgc ttc gtg ccc tac aac agc acg ctg gcg gtc tac ggg ctg ctg	1061
Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val Tyr Gly Leu Leu	
245 250 255 260	
cgg agc aag ctg gtg gcg gcc agc gtg cct gcc cgc gat cgc gtg cgc	1109
Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg Asp Arg Val Arg	
265 270 275	
ggg gtg ctg atg gtg atg gtg ctg ctg gcc gcc gcc aac tgc gtg ctg	1157

Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala Asn Cys Val Leu	
280 285 290	
gac ccg ctg gtg tac tac ttt agc gcc gag ggc ttc cgc aac acc ctg	1205
Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe Arg Asn Thr Leu	
295 300 305	
cgc ggc ctg ggc act ccg cac cgg gcc agg acc tcg gcc acc aac ggg	1253
Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser Ala Thr Asn Gly	
310 315 320	
acg cgg gcg gcg ctc gcg caa tcc gaa agg tcc gcc gtc acc acc gac	1301
Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala Val Thr Thr Asp	
325 330 335 340	
gcc acc agg ccg gat gcc gcc agt cag ggg ctg ctc cga ccc tcc gac	1349
Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu Arg Pro Ser Asp	
345 350 355	
tcc cac tct ctg tct tcc ttc aca cag tgt ccc cag gat tcc gcc ctc	1397
Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln Asp Ser Ala Leu	
360 365 370	
tga acacacatgc cattgcgctg tccgtgcccg actcccaacg cctctcgttc	1450
tgggaggctt acaggggtgta cacacaagaa ggtgggctgg gcacttggac ctttgggtgg	1510
caattccagc ttagcaacgc agaagagtac aaagtgtgga agccagggcc cagggaaggc	1570
agtgtctgctg gaaatggctt ctttaaactg tgagcacgca gagcaccct tctccagcgg	1630
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<210> 26

<211> 2237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)...(465)

<400> 26

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Gly Ala Ala Ala Leu Gly Gly Ala Leu Phe Leu Leu Leu Phe Ala Leu	
10 15 20 25	
ggg gtc cgc cag ctg ctg aag cag agg cgg ccg atg ggc ttc ccc ccg	147
Gly Val Arg Gln Leu Leu Lys Gln Arg Arg Pro Met Gly Phe Pro Pro	
30 35 40	
ggg ccg ccg ggg ctg cca ttt atc ggc aac atc tat tcc ctg gca gcc	195
Gly Pro Pro Gly Leu Pro Phe Ile Gly Asn Ile Tyr Ser Leu Ala Ala	
45 50 55	
tca tcc gag ctt ccc cat gtc tac atg aga aag cag agc cag gtg tac	243
Ser Ser Glu Leu Pro His Val Tyr Met Arg Lys Gln Ser Gln Val Tyr	
60 65 70	
gga gag gta cag ccc cga cgg gcc ccg ggc agg gag ggc cgc cag gct	291
Gly Glu Val Gln Pro Arg Arg Ala Pro Gly Arg Glu Gly Arg Gln Ala	
75 80 85	
ggc ccg ggc tgg cca ggg cct tcc tgg ttg gac tta tgg ccg ccc ctg	339
Gly Pro Gly Trp Pro Gly Pro Ser Trp Leu Asp Leu Trp Pro Pro Leu	
90 95 100 105	
ggc cga cta gtc ggg acc tct ccg tgt gcc ggc tgc cct ttg agg gac	387
Gly Arg Leu Val Gly Thr Ser Pro Cys Ala Gly Cys Pro Leu Arg Asp	
110 115 120	
acc cgc ttc ccg ggt ctg gaa ggg aga agt cct cga cgc cgt gcc ccc	435
Thr Arg Phe Pro Gly Leu Glu Gly Arg Ser Pro Arg Arg Arg Ala Pro	
125 130 135	

ttg cag ggg gag ccc cgc ccc tgc cgg tgaccactc cgggcca 480

Leu Gln Gly Glu Pro Arg Pro Cys Arg

140

145

ggctccgagg cgatccagtc ctgattttcc cgctaccgct cgagctcttg ctctgcgcc 540

tgcgccgttt ggctcgccag ccgcgcgcc acttcaggtc cagggtggac gcatgccctc 600

aggtgcgggc gtcttgcgag tcggcctcgc agctctgttg aagctgcacg cggcttgctg 660

gaaaatcaag gcgttctgag ttctagatgg ttaatagcag gttcttcggg gtctgcagtc 720

gacgaacgac tgggtgtaggc gtttgctgtg agaatggaga atgcagggga acgcccctga 780

ctgagaagcg ggccctggga aacgattgtg aacgcgtgaa tgaattgatg actaaaatcc 840

gctgcggggg tcttacagcg cagatggtaa tgccgttctg actggctggg aacggcacct 900

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ttaaaactca taaccagccg gtgaggctcg tacttcgctc ctctcattc tgcggagggg 1020

aaagcagcac ggaaatgcc tgtgactggc agcggaaaag gcgaccaccg cttgtgtatc 1080

ttcagtttag atcttgagg catatcaact gtggttctaa atggctatga tgtagtaaag 1140

gaatgccttg ttcataaaag cgaaattttt gcagacagac catgccttcc tttattcatg 1200

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aaaatcttgg aagaaaccaa atttttcaat gatgctattg aaacatacaa aggtagacct 1380

tttgacttta aacagttaat aacgaatgct gtttcaaaca taaccaatct gatcattttt 1440

ggagaacgat tcacttatga agacaccgat tttcagcaca tgattgagtt atttagtgaa 1500

aatgtggaac tagctgccag tgccctcagtc ttcttgata atgcctttcc atggattggc 1560

atctgcctt ttggaaaaca tcaacagctg tttagaaatg cagctgtagt ctatgatttt 1620

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gttgatgctt atttagatga gatggatcaa ggtaaaaatg acccatcatc tactttctcc 1740

aaagaaaacc taattttctc agtgggtgaa ctcatcattg ctggaactga aactacaacc 1800

aatgtgctac ggtgggcgat tcttttcatg gccctttatc ctaatattca agtactggag 1860

agaccagaa gtgttccatc ctgagcgatt tctggacagc agtggatatt ttgccaagaa 1920

ggaagctttg gttccttttt ccctaggaag aagacattgt cttggagaac acttggctcg 1980

gatggaaatg ttcttgtttt ttacagcatt gcttcagagg tttcatttgc attttccaca 2040

tgaactagtt ccagatctga agcccagggt aggcattgaca ttgcagcccc aaccctacct 2100

catctgtgct gaaagacgct gaaactgcct gggatgtttt cgggaacaag aatgtatatt 2160
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 catcaaaaag ccaaattg 2237

<210> 27

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (268)...(1176)

<400> 27

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 aatctggaag ggcgggtgaaa aacctacgtc ctgccctcgc ccggcctctc cattcgcccc 180
 ccgggtagag aggtgcccgg ctcccacccc ttcccagccc cagccctgga gacagcagcc 240
 cctagactac tgagggacag cgacagc atg aag gct ccg ggt cgg ctc gtg 291

Met Lys Ala Pro Gly Arg Leu Val

1 5

ctc atc atc ctg tgc tcc gtg gtc ttc tct gcc gtc tac atc ctc ctg 339
 Leu Ile Ile Leu Cys Ser Val Val Phe Ser Ala Val Tyr Ile Leu Leu

10 15 20

tgc tgc tgg gcc ggc ctg ccc ctc tgc ctg gcc acc tgc ctg gac cac 387
 Cys Cys Trp Ala Gly Leu Pro Leu Cys Leu Ala Thr Cys Leu Asp His

25 30 35 40

cac ttc ccc aca ggc tcc agg ccc act gtg ccg gga ccc ctg cac ttc 435
 His Phe Pro Thr Gly Ser Arg Pro Thr Val Pro Gly Pro Leu His Phe

45 50 55

agt gga tat agc agt gtg cca gat ggg aag ccg ctg gtc cgc gag ccc	483
Ser Gly Tyr Ser Ser Val Pro Asp Gly Lys Pro Leu Val Arg Glu Pro	
60 65 70	
tgc cgc agc tgt gcc gtg gtg tcc agc tcc ggc caa atg ctg ggc tca	531
Cys Arg Ser Cys Ala Val Val Ser Ser Ser Gly Gln Met Leu Gly Ser	
75 80 85	
ggc ctg ggt gct gag atc gac agt gcc gag tgc gtg ttc cgc atg aac	579
Gly Leu Gly Ala Glu Ile Asp Ser Ala Glu Cys Val Phe Arg Met Asn	
90 95 100	
cag gcg ccc acc gtg ggc ttt gag gcg gat gtg ggc cag cgc agc acc	627
Gln Ala Pro Thr Val Gly Phe Glu Ala Asp Val Gly Gln Arg Ser Thr	
105 110 115 120	
ctg cgt gtc gtc tca cac aca agc gtg ccg ctg ctg ctg cgc aac tat	675
Leu Arg Val Val Ser His Thr Ser Val Pro Leu Leu Leu Arg Asn Tyr	
125 130 135	
tca cac tac ttc cag aag gcc cga gac acg ctc tac atg gtg tgg ggc	723
Ser His Tyr Phe Gln Lys Ala Arg Asp Thr Leu Tyr Met Val Trp Gly	
140 145 150	
cag ggc agg cac atg gac cgg gtg ctc ggc ggc cgc acc tac cgc acg	771
Gln Gly Arg His Met Asp Arg Val Leu Gly Gly Arg Thr Tyr Arg Thr	
155 160 165	
ctg ctg cag ctc acc agg atg tac ccc ggc ctg cag gtg tac acc ttc	819
Leu Leu Gln Leu Thr Arg Met Tyr Pro Gly Leu Gln Val Tyr Thr Phe	
170 175 180	
acg gag cgc atg atg gcc tac tgc gac cag atc ttc cag gac gag acg	867
Thr Glu Arg Met Met Ala Tyr Cys Asp Gln Ile Phe Gln Asp Glu Thr	
185 190 195 200	
ggc aag aac cgg agg cag tcg ggc tcc ttc ctc agc acc ggc tgg ttc	915
Gly Lys Asn Arg Arg Gln Ser Gly Ser Phe Leu Ser Thr Gly Trp Phe	
205 210 215	

acc atg atc ctc gcg ctg gag ctg tgt gag gag atc gtg gtc tat ggg	963
Thr Met Ile Leu Ala Leu Glu Leu Cys Glu Glu Ile Val Val Tyr Gly	
220 225 230	
atg gtc agc gac agc tac tgc agg gag aag agc cac ccc tca gtg cct	1011
Met Val Ser Asp Ser Tyr Cys Arg Glu Lys Ser His Pro Ser Val Pro	
235 240 245	
tac cac tac ttt gag aag ggc cgg cta gat gag tgt cag atg tac ctg	1059
Tyr His Tyr Phe Glu Lys Gly Arg Leu Asp Glu Cys Gln Met Tyr Leu	
250 255 260	
gca cac gag cag gcg ccc cga agc gcc cac cgc ttc atc act gag aag	1107
Ala His Glu Gln Ala Pro Arg Ser Ala His Arg Phe Ile Thr Glu Lys	
265 270 275 280	
gcg gtc ttc tcc cgc tgg gcc aag aag agg ccc atc gtg ttc gcc cat	1155
Ala Val Phe Ser Arg Trp Ala Lys Lys Arg Pro Ile Val Phe Ala His	
285 290 295	
ccg tcc tgg agg act gag tagcttccgt cgtcctgccca gccgccatgc cgttgcg	1210
Pro Ser Trp Arg Thr Glu	
300	
aggcctccgg gatgtcccat cccaagccat cacactccac aaaaacattt aatttatgga	1270
tcttgccctcc tgccacgtgc tgggtggacc taaggttcct tcccgcccca ttctggcgac	1330
acttgagacc atctcaggcc tcatgacttg aaggggagtg gaggggggag ccgtgtctcc	1390
ccctccact cctgagtaa ttcattggcat ttgggggctc accccacctc caggtctgtc	1450
aagtggcctt tgtccctggg gctgatggcc cccaactcac cagcatcatg accttggtcc	1510
agtctgggtc ctccctcccc agccgcccct accacctttt ggtgccacac ttctcaggct	1570
ggccgcccctg gttggggcag ccgagagcct ggggttcatt ggtgaagggg ccttgaggtt	1630
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<210> 28

<211> 963

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (246)...(830)

<400> 28

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agaaaaattg atgaactgaa gaagacatgg tccattatgc cttacaaact tacacagtgc      180
tttggaatt ccaaagtact cagtggagag aggtgtttca ggagccgtag agccagatcg      240
tcatc atg tct gca ttg tgg ctg ctg ctg ggc ctc ctt gcc ctg atg      287
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Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met

1 5 10

```
gac ttg tct gaa agc agc aac tgg gga tgc tat gga aac atc caa agc      335
Asp Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser
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15 20 25 30

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ctg gac acc cct gga gca tct tgt ggg att gga aga cgt cac ggc ctg      383
Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu
```

35 40 45

```
aac tac tgt gga gtt cgt gct tct gaa agg ctg gct gaa ata gac atg      431
Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met
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50 55 60

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cca tac ctc ctg aaa tat caa ccc atg atg caa acc att ggc caa aag      479
Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys
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65 70 75

```
tac tgc atg gat cct gcc gtg atc gct ggt gtc ttg tcc agg aag tct      527
Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser
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80 85 90

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ccc ggt gac aaa att ctg gtc aac atg ggc gat agg act agc atg gtg      575
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<222> (229)...(1857)

<400> 29

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gatggtgagg catcatgcta gggagctgag ctctgacctt cctgctgggt gattctccac 180
ctctgggctg ctagatctac ttcttgatg cctgaagat cctcatgt atg aaa 234

Met Lys

1

atg aag tcc cag gca acc atg att tgc tgc tta gtg ttc ttt ctg tcc 282
Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe Leu Ser

5

10

15

aca gaa tgt tcc cac tat aga tcc aag att cac cta aaa agc tat agt 330
Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser Tyr Ser

20

25

30

gaa gtg gcc aac cac atc ctc gac aca gca gcc att tca aac tgg gct 378
Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala

35

40

45

50

ttc att ccc aac aaa aat gcc agc tcg gat ttg ttg cag tca gtg aat 426
Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn

55

60

65

ttg ttt gcc aga caa ctc cac atc cac aat aat tct gag aac att gtg 474
Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val

70

75

80

aat gaa ctc ttc att cag aca aaa ggg ttt cac atc aac cat aat acc 522
Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr

85

90

95

tca gag aaa agc ctc aat ttc tcc atg agc atg aac aat acc aca gaa 570
Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu

100

105

110

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Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu	
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Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala	
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Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn	
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Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser	
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Val	Asn	Ile	Ala	Val	Ser	Leu	Leu	Thr	Ala	Asn	Val	Trp	Phe	Ile	Ile	
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Gly	Ser	His	Phe	Asn	Ile	Lys	Ala	Gln	Asp	Tyr	Asn	Met	Cys	Val	Ala	
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Val	Thr	Phe	Phe	Ser	His	Phe	Phe	Tyr	Leu	Ser	Leu	Phe	Phe	Trp	Met	
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Leu	Phe	Lys	Ala	Leu	Leu	Ile	Ile	Tyr	Gly	Ile	Leu	Val	Ile	Phe	Arg	
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Arg	Met	Met	Lys	Ser	Arg	Met	Met	Val	Ile	Gly	Phe	Ala	Ile	Gly	Tyr	
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Gly	Cys	Pro	Leu	Ile	Ile	Ala	Val	Thr	Thr	Val	Ala	Ile	Thr	Glu	Pro	
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Glu	Asn	Gly	Tyr	Met	Arg	Pro	Glu	Ala	Cys	Trp	Leu	Asn	Trp	Asp	Asn	
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acc	aaa	gcc	ctt	tta	gca	ttt	gcc	atc	ccg	gcg	ttc	gtc	att	gtg	gct	1482
Thr	Lys	Ala	Leu	Leu	Ala	Phe	Ala	Ile	Pro	Ala	Phe	Val	Ile	Val	Ala	
			405					410						415		
gta	aat	ctg	att	gtg	gtt	ttg	gtt	gtt	gct	gtc	aac	act	cag	agg	ccc	1530
Val	Asn	Leu	Ile	Val	Val	Leu	Val	Val	Ala	Val	Asn	Thr	Gln	Arg	Pro	
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Met

1

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 Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu Leu

5

10

15

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20

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Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser Arg	
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Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro Gln	
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Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp Gln	
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Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn Ala	
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Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met Asp	
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Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile Thr	
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Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro Ser	
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